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## Entry information

Entry name **SPB7\_HUMAN**  
 Primary accession number **O75635**  
 Secondary accession numbers None  
 Entered in Swiss-Prot in Release 41, February 2003  
 Sequence was last modified in Release 41, February 2003  
 Annotations were last modified in Release 41, February 2003

## Name and origin of the protein

Protein name **Megsin**  
 Synonyms **TP55**  
**Serpin B7**  
 Gene name **SERPINB7**  
 From **Homo sapiens (Human) [TaxID: 9606]**  
 Taxonomy **[Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#); [Mammalia](#); [Eutheria](#); [Primates](#); [Catarrhini](#); [Hominidae](#); [Homo](#).**

## References

### [1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=97326116; PubMed=9182567; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
[Tsuji moto M.](#), [Tsuruoka N.](#), [Ishida N.](#), [Kurihara T.](#), [Iwasa F.](#), [Yamashiro K.](#), [Rogi T.](#), [Kodama S.](#),  
[Katsuragi N.](#), [Adachi M.](#), [Katayama T.](#), [Nakao M.](#), [Yamaichi K.](#), [Hashino J.](#), [Haruyama M.](#), [Miura K.](#),  
[Nakanishi T.](#), [Nakazato H.](#), [Teramura M.](#), [Mizoguchi H.](#), [Yamaguchi N.](#);  
 "Purification, cDNA cloning, and characterization of a new serpin with megakaryocyte maturation activity.";  
[J. Biol. Chem.](#) 272:15373-15380(1997).

### [2] SEQUENCE FROM NUCLEIC ACID.

TISSUE=[Mesangial cells](#);  
 MEDLINE=98376492; PubMed=9710452; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
[Miyata T.](#), [Nangaku M.](#), [Suzuki D.](#), [Inagi R.](#), [Uragami K.](#), [Sakai H.](#), [Okubo K.](#), [Kurokawa K.](#);  
 "A mesangium-predominant gene, megsin, is a new serpin upregulated in IgA nephropathy.";  
[J. Clin. Invest.](#) 102:828-836(1998).

## Comments

- **FUNCTION:** Might function as an inhibitor of Lys-specific proteases. Might influence the maturation of megakaryocytes via its action as a serpin.

- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **TISSUE SPECIFICITY:** Predominantly expressed in mesangial cells.
- **SIMILARITY:** Belongs to the serpin family. Ov-serpin subfamily.

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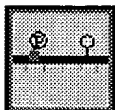
### Cross-references

EMBL	D88575; BAA31232.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ] AF027866; AAC64506.1; -. [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
HSSP	P05619; 1HLE. [ <a href="#">HSSP ENTRY</a> / <a href="#">PDB</a> ]
Genew	<a href="#">HGNC:13902</a> ; SERPINB7.
CleanEx	<a href="#">HGNC:13902</a> ; SERPINB7.
MIM	603357 [ <a href="#">NCBI</a> / <a href="#">EBI</a> ].
GeneCards	<a href="#">SERPINB7</a> .
GeneLynx	<a href="#">SERPINB7</a> ; Homo sapiens.
GO	<a href="#">GO:0004868</a> ; Molecular function: serpin ( <i>traceable author statement</i> ).
SOURCE	<a href="#">SERPINB7</a> ; Homo sapiens.
Ensembl	O75635; Homo sapiens. [ <a href="#">Entry</a> / <a href="#">Contig view</a> ]
InterPro	<a href="#">IPR000215</a> ; Serpin. <a href="#">Graphical view of domain structure</a> .
Pfam	<a href="#">PF00079</a> ; serpin; 1.
SMART	<a href="#">SM00093</a> ; SERPIN; 1.
PROSITE	<a href="#">PS00284</a> ; SERPIN; 1.
ProDom	[ <a href="#">Domain structure</a> / <a href="#">List of seq. sharing at least 1 domain</a> ]
HOVERGEN	[ <a href="#">Family</a> / <a href="#">Alignment</a> / <a href="#">Tree</a> ]
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ProtoNet	<a href="#">O75635</a> .
ProtoMap	<a href="#">O75635</a> .
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### Keywords

**Serpin**; **Serine protease inhibitor**.

### Features



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Key	From	To	Length	Description
ACT_SITE	347	348		REACTIVE BOND ( <i>BY SIMILARITY</i> ) .

### Sequence information

Length: **380** Molecular weight: **42904** CRC64: **9A2CDB6C63CFF605** [This is a checksum on the  
AA Da sequence]

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      70      80      90     100     110     120
      |      |      |      |      |      |
NTASGYGNSS NSQSGLQSQL KRVFSDINAS HKDYDLSIVN GLFAEKVYGF HKDYIECAEK

     130     140     150     160     170     180
      |      |      |      |      |      |
LYDAKVERVD FTNHLEDTRR NINKWVENET HGKIKNVIGE GGISSSAVMV LVNAVYFKGK

     190     200     210     220     230     240
      |      |      |      |      |      |
WQSAFTKSET INCHFKSPKC SGKAVAMHQ ERKFNLVIE DPSMKILELR YNGGINMYVL

     250     260     270     280     290     300
      |      |      |      |      |      |
LPENDLSEIE NKLTFQNLME WTNPRRMTSK YVEVFFPQFK IEKNYEMKQY LRALGLKDIF

     310     320     330     340     350     360
      |      |      |      |      |      |
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     370     380
      |      |
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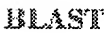
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